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1600

RAW SEQUENCE LISTING

DATE: 02/12/2003

PATENT APPLICATION: US/08/783,734D

TIME: 11:15:26

Input Set : A:\EP.txt

Output Set: N:\CRF4\02112003\H783734D.raw

3 <110> APPLICANT: Friedman, Jeffrey M.
 4 Lee, Gwo-Hua
 5 Proenca, Ricardo
 6 Ioffe, Ella
 8 <120> TITLE OF INVENTION: DB, THE RECEPTOR FOR LEPTIN, NUCLEIC ACIDS ENCODING THE
 RECEPTOR, AND

p.6

ENTERED

9 USES THEREOF
 11 <130> FILE REFERENCE: 600-1-162CP2
 13 <140> CURRENT APPLICATION NUMBER: US 08/783,734D
 14 <141> CURRENT FILING DATE: 1997-01-16
 16 <150> PRIOR APPLICATION NUMBER: US 08/599,974
 17 <151> PRIOR FILING DATE: 1996-02-14
 19 <150> PRIOR APPLICATION NUMBER: US 08/586,594
 20 <151> PRIOR FILING DATE: 1996-01-16
 22 <160> NUMBER OF SEQ ID NOS: 126
 24 <170> SOFTWARE: PatentIn version 3.1
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 2529
 28 <212> TYPE: DNA
 29 <213> ORGANISM: Mus musculus
 31 <400> SEQUENCE: 1
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 34 ccatgccgga tcagcaccag ctgtagctc gtgccgaatt cggcacgagg ttgctttggg 120
 36 aatgagcaag gtcaaaactg ctctgcactc acagacaaca ctgaaggga gacactggct 180
 38 tcagtagtga aggcttcagt ttttcgccag ctagggtgtaa actgggacat agagtgtctg 240
 40 atgaaagggg acttgacatt attcatctgt catatggagc cattacctaa gaacccttc 300
 42 aagaattatg actctaaggt ccatctttta tatgatctgc ctgaagtcac agatgattcg 360
 44 cctctgcccc cactgaaaga cagctttcag actgtccaat gcaactgcag tcttcgggga 420
 46 tgtgaatgtc atgtgccggg acccagagcc aaactcaact acgctcttct gatgtatttg 480
 48 gaaatcacat ctgccgggtg gagttttcag tcacctctga tgtcactgca gcccattgctt 540
 50 gttgtgaaac ccgatccacc cttaggtttg catatggaag tcacagatga tggtaattta 600
 52 aagatttctt gggacagcca aacaatggca ccatttcgcg ttcaatatca ggtgaaatat 660
 54 ttagagaatt ctacaattgt aagagaggct gctgaaattg tctcagctac atctctgctg 720
 56 gtagacagtg tgcttcctgg atcttcatat gaggtccagg tgaggagcaa gagactggat 780
 58 gggttcaggag tctggagtga ctggagttca cctcaagtct ttaccacaca agatgtttgtg 840
 60 tattttccac ccaaaattct gactagtgtt ggatcgaatg cttcttttca ttgcatctac 900
 62 aaaaacgaaa accagattat ctctcaaaa cagatagttt ggtggaggaa tctagctgag 960
 64 aaaatccctg agatacagta cagcattgtg agtgaccgag ttagcaaagt taccttctcc 1020
 66 aacctgaaag ccaccagacc tcgagggaag ttacctatg acgcagtgtg ctgctgcaat 1080
 68 gagcaggcgt gccatcaccg ctatgctgaa ttatacgtga tcgatgtcaa tatcaatata 1140
 70 tcatgtgaaa ctgacgggta cttactaaa atgacttgca gatggtcacc cagcacaatc 1200
 72 caatcactag tgggaagcac tgtgcagctg aggtatcaca ggcgcagcct gtattgtcct 1260
 74 gatagtccat ctattcatcc tacgtctgag cccaaaaact gcgtcttaca gagagacggc 1320
 76 ttttatgaat gtgttttcca gccaatcttt ctattatctg gctatacaat gtggatcagg 1380

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78 atcaaccatt ctttaggttc acttgactcg ccaccaacgt gtgtccttcc tgactccgta 1440
80 gtaaaaccac tacctccatc taacgtaaaa gcagagatta ctgtaaacac tggattattg 1500
82 aaagtatctt gggaaaagcc agtccttccg gagaataacc ttcaattcca gattcgatat 1560
84 ggcttaagtg gaaaagaaat acaatggaag acacatgagg tattcgatgc aaagtcaaaag 1620
86 tctgccagcc tgctggtgtc agacctctgt gcagctctatg tgggccaggt tcgctgccgg 1680
88 cggttggatg gactaggata ttggagtaat tggagcagtc cagcctatac gcttgtcatg 1740
90 gatgtaaaag ttctatgag agggcctgaa ttttggagaa aaatggatgg ggacgttact 1800
92 aaaaaggaga gaaatgtcac ctgtctttgg aagcccctga cgaaaaatga ctcactgtgt 1860
94 agtgtgagga ggtacgtggt gaagcatcgt actgcccaca atgggacgtg gtcagaagat 1920
96 gtgggaaatc ggaccaatct cactttcctg tggacagaac cagcgcacac tgttacagtt 1980
98 ctggctgtca attccctcgg cgcttccctt gtgaatttta accttacctt ctcatggccc 2040
100 atgagtaaag tgagtgtgtt ggagtcactc agtgcttata ccctgagcag cagctgtgtc 2100
102 atcctttcct ggacactgtc acctgatgat tatagtctgt tatatctggt tattgaatgg 2160
104 aagatcctta atgaagatga tggaaatgaag tggcttagaa ttccctcgaa tgttaaaaaag 2220
106 ttttatatcc acgataatct tattcccatc gagaaatata agtttagtct ttaccagta 2280
108 tttatggaag gagttggaaa accaaagata attaattggt tcaccaaaga tgctatcgac 2340
110 aagcagcaga atgacgcagg gctgtatgtc attgtaccca taattatttc ctctgtgtc 2400
112 ctactgctcg gaacactggt aatttcacac cagagaatga aaaagtgtt ttgggacgat 2460
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116 actctttga

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119 <210> SEQ ID NO: 2

120 <211> LENGTH: 842

121 <212> TYPE: PRT

122 <213> ORGANISM: Mus musculus

124 <220> FEATURE:

125 <221> NAME/KEY: MISC_FEATURE

126 <222> LOCATION: (29)..(29)

127 <223> OTHER INFORMATION: X can be any amino acid

130 <400> SEQUENCE: 2

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132 Gly Leu Arg Ser Ala Ser Tyr Gln Pro Leu Lys Arg Phe Ser Arg Phe
133 1 5 10 15
W--> 136 Gln Ala Leu Ser Pro Cys Arg Ile Ser Thr Ser Leu Xaa Leu Val Pro
137 20 25 30
140 Asn Ser Ala Arg Gly Cys Phe Gly Asn Glu Gln Gly Gln Asn Cys Ser
141 35 40 45
144 Ala Leu Thr Asp Asn Thr Glu Gly Lys Thr Leu Ala Ser Val Val Lys
145 50 55 60
148 Ala Ser Val Phe Arg Gln Leu Gly Val Asn Trp Asp Ile Glu Cys Trp
149 65 70 75 80
152 Met Lys Gly Asp Leu Thr Leu Phe Ile Cys His Met Glu Pro Leu Pro
153 85 90 95
156 Lys Asn Pro Phe Lys Asn Tyr Asp Ser Lys Val His Leu Leu Tyr Asp
157 100 105 110
160 Leu Pro Glu Val Ile Asp Asp Ser Pro Leu Pro Pro Leu Lys Asp Ser
161 115 120 125
164 Phe Gln Thr Val Gln Cys Asn Cys Ser Leu Arg Gly Cys Glu Cys His
165 130 135 140
168 Val Pro Val Pro Arg Ala Lys Leu Asn Tyr Ala Leu Leu Met Tyr Leu
169 145 150 155 160

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172 Glu Ile Thr Ser Ala Gly Val Ser Phe Gln Ser Pro Leu Met Ser Leu
173                               165                               170                               175
176 Gln Pro Met Leu Val Val Lys Pro Asp Pro Pro Leu Gly Leu His Met
177                               180                               185                               190
180 Glu Val Thr Asp Asp Gly Asn Leu Lys Ile Ser Trp Asp Ser Gln Thr
181                               195                               200                               205
184 Met Ala Pro Phe Pro Leu Gln Tyr Gln Val Lys Tyr Leu Glu Asn Ser
185                               210                               215                               220
188 Thr Ile Val Arg Glu Ala Ala Glu Ile Val Ser Ala Thr Ser Leu Leu
189 225                               230                               235                               240
192 Val Asp Ser Val Leu Pro Gly Ser Ser Tyr Glu Val Gln Val Arg Ser
193                               245                               250                               255
196 Lys Arg Leu Asp Gly Ser Gly Val Trp Ser Asp Trp Ser Ser Pro Gln
197                               260                               265                               270
200 Val Phe Thr Thr Gln Asp Val Val Tyr Phe Pro Pro Lys Ile Leu Thr
201                               275                               280                               285
204 Ser Val Gly Ser Asn Ala Ser Phe His Cys Ile Tyr Lys Asn Glu Asn
205                               290                               295                               300
208 Gln Ile Ile Ser Ser Lys Gln Ile Val Trp Trp Arg Asn Leu Ala Glu
209 305                               310                               315                               320
212 Lys Ile Pro Glu Ile Gln Tyr Ser Ile Val Ser Asp Arg Val Ser Lys
213                               325                               330                               335
216 Val Thr Phe Ser Asn Leu Lys Ala Thr Arg Pro Arg Gly Lys Phe Thr
217                               340                               345                               350
220 Tyr Asp Ala Val Tyr Cys Cys Asn Glu Gln Ala Cys His His Arg Tyr
221                               355                               360                               365
224 Ala Glu Leu Tyr Val Ile Asp Val Asn Ile Asn Ile Ser Cys Glu Thr
225                               370                               375                               380
228 Asp Gly Tyr Leu Thr Lys Met Thr Cys Arg Trp Ser Pro Ser Thr Ile
229 385                               390                               395                               400
232 Gln Ser Leu Val Gly Ser Thr Val Gln Leu Arg Tyr His Arg Arg Ser
233                               405                               410                               415
236 Leu Tyr Cys Pro Asp Ser Pro Ser Ile His Pro Thr Ser Glu Pro Lys
237                               420                               425                               430
240 Asn Cys Val Leu Gln Arg Asp Gly Phe Tyr Glu Cys Val Phe Gln Pro
241                               435                               440                               445
244 Ile Phe Leu Leu Ser Gly Tyr Thr Met Trp Ile Arg Ile Asn His Ser
245                               450                               455                               460
248 Leu Gly Ser Leu Asp Ser Pro Pro Thr Cys Val Leu Pro Asp Ser Val
249 465                               470                               475                               480
252 Val Lys Pro Leu Pro Pro Ser Asn Val Lys Ala Glu Ile Thr Val Asn
253                               485                               490                               495
256 Thr Gly Leu Leu Lys Val Ser Trp Glu Lys Pro Val Phe Pro Glu Asn
257                               500                               505                               510
260 Asn Leu Gln Phe Gln Ile Arg Tyr Gly Leu Ser Gly Lys Glu Ile Gln
261                               515                               520                               525
264 Trp Lys Thr His Glu Val Phe Asp Ala Lys Ser Lys Ser Ala Ser Leu
265                               530                               535                               540
268 Leu Val Ser Asp Leu Cys Ala Val Tyr Val Val Gln Val Arg Cys Arg

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269 545          550          555          560
272 Arg Leu Asp Gly Leu Gly Tyr Trp Ser Asn Trp Ser Ser Pro Ala Tyr
273          565          570          575
276 Thr Leu Val Met Asp Val Lys Val Pro Met Arg Gly Pro Glu Phe Trp
277          580          585          590
280 Arg Lys Met Asp Gly Asp Val Thr Lys Lys Glu Arg Asn Val Thr Leu
281          595          600          605
284 Leu Trp Lys Pro Leu Thr Lys Asn Asp Ser Leu Cys Ser Val Arg Arg
285          610          615          620
288 Tyr Val Val Lys His Arg Thr Ala His Asn Gly Thr Trp Ser Glu Asp
289 625          630          635          640
292 Val Gly Asn Arg Thr Asn Leu Thr Phe Leu Trp Thr Glu Pro Ala His
293          645          650          655
296 Thr Val Thr Val Leu Ala Val Asn Ser Leu Gly Ala Ser Leu Val Asn
297          660          665          670
300 Phe Asn Leu Thr Phe Ser Trp Pro Met Ser Lys Val Ser Ala Val Glu
301          675          680          685
304 Ser Leu Ser Ala Tyr Pro Leu Ser Ser Ser Cys Val Ile Leu Ser Trp
305          690          695          700
308 Thr Leu Ser Pro Asp Asp Tyr Ser Leu Leu Tyr Leu Val Ile Glu Trp
309 705          710          715          720
312 Lys Ile Leu Asn Glu Asp Asp Gly Met Lys Trp Leu Arg Ile Pro Ser
313          725          730          735
316 Asn Val Lys Lys Phe Tyr Ile His Asp Asn Phe Ile Pro Ile Glu Lys
317          740          745          750
320 Tyr Gln Phe Ser Leu Tyr Pro Val Phe Met Glu Gly Val Gly Lys Pro
321          755          760          765
324 Lys Ile Ile Asn Gly Phe Thr Lys Asp Ala Ile Asp Lys Gln Gln Asn
325          770          775          780
328 Asp Ala Gly Leu Tyr Val Ile Val Pro Ile Ile Ile Ser Ser Cys Val
329 785          790          795          800
332 Leu Leu Leu Gly Thr Leu Leu Ile Ser His Gln Arg Met Lys Lys Leu
333          805          810          815
336 Phe Trp Asp Asp Val Pro Asn Pro Lys Asn Cys Ser Trp Ala Gln Gly
337          820          825          830
340 Leu Asn Phe Gln Lys Arg Thr Asp Thr Leu
341          835          840
344 <210> SEQ ID NO: 3
345 <211> LENGTH: 2848
346 <212> TYPE: DNA
347 <213> ORGANISM: Mus musculus
349 <220> FEATURE:
350 <221> NAME/KEY: misc_feature /
351 <222> LOCATION: (44)..(44)
352 <223> OTHER INFORMATION: N can be A, C, T or G
355 <220> FEATURE:
356 <221> NAME/KEY: misc_feature
357 <222> LOCATION: (67)..(67)
358 <223> OTHER INFORMATION: N can be A, C, T or G

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Input Set : A:\EP.txt

Output Set: N:\CRF4\02112003\H783734D.raw

361 <220> FEATURE:
362 <221> NAME/KEY: misc_feature
363 <222> LOCATION: (234)..(234)
364 <223> OTHER INFORMATION: N can be A, C, T or G
367 <220> FEATURE:
368 <221> NAME/KEY: misc_feature
369 <222> LOCATION: (483)..(483)
370 <223> OTHER INFORMATION: N can be A, C, T or G
373 <220> FEATURE:
374 <221> NAME/KEY: misc_feature
375 <222> LOCATION: (527)..(527)
376 <223> OTHER INFORMATION: N can be A, C, T or G
379 <220> FEATURE:
380 <221> NAME/KEY: misc_feature
381 <222> LOCATION: (564)..(564)
382 <223> OTHER INFORMATION: N can be A, C, T or G
385 <220> FEATURE:
386 <221> NAME/KEY: misc_feature
387 <222> LOCATION: (1237)..(1237)
388 <223> OTHER INFORMATION: N can be A, C, T or G
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393 <222> LOCATION: (1335)..(1335)
394 <223> OTHER INFORMATION: N can be A, C, T or G
397 <220> FEATURE:
398 <221> NAME/KEY: misc_feature
399 <222> LOCATION: (2038)..(2038)
400 <223> OTHER INFORMATION: N can be A, C, T or G
403 <220> FEATURE:
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405 <222> LOCATION: (2179)..(2179)
406 <223> OTHER INFORMATION: N can be A, C, T or G
409 <220> FEATURE:
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411 <222> LOCATION: (2182)..(2182)
412 <223> OTHER INFORMATION: N can be A, C, T or G
415 <220> FEATURE:
416 <221> NAME/KEY: misc_feature
417 <222> LOCATION: (2183)..(2183)
418 <223> OTHER INFORMATION: N can be A, C, T or G
421 <220> FEATURE:
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423 <222> LOCATION: (2219)..(2219)
424 <223> OTHER INFORMATION: N can be A, C, T or G
427 <220> FEATURE:
428 <221> NAME/KEY: misc_feature
429 <222> LOCATION: (2576)..(2576)
430 <223> OTHER INFORMATION: N can be A, C, T or G
433 <220> FEATURE:

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; Xaa Pos. 29
Seq#:3; N Pos. 44,67,234,483,527,564,1237,1335,2038,2179,2182,2183,2219
Seq#:3; N Pos. 2576,2610
Seq#:4; Xaa Pos. 79
Seq#:5; N Pos. 160,258
Seq#:6; Xaa Pos. 14,19,25,58,67,68,84,86
Seq#:35; N Pos. 5
Seq#:39; N Pos. 55,62,72,143
Seq#:40; N Pos. 83,101,181
Seq#:41; N Pos. 193
Seq#:86; Xaa Pos. 29
Seq#:87; Xaa Pos. 29
Seq#:88; Xaa Pos. 29
Seq#:89; Xaa Pos. 79
Seq#:90; Xaa Pos. 14,19,25,58,67,68,84,86
Seq#:91; Xaa Pos. 79
Seq#:92; Xaa Pos. 14,19,25,58,67,68,84,86